# Appendix II

### P03170US/WARF-0204

SOURDERS GIRDOR

	351	PLAAKTLGGILCFKREERAWEHVRDSPTWNLPQDESSILPALSLSYHQLP	400
5	351	PLAAKTLGGILCPKREERAWEHVRDSPIWNLPQDESSILPALRLSYHQLP	400
	401	LDLKOCFAYCAVFPKOAKMEKEKLISTMMANGFLLSKGNMELEDVGDEVW	450
	801	LDLKQCFAYCAVFFKDAKMKKEKLISTMMAHGFLLSKGNMELEDVGDBVW	450
10	451	EKL*LRSFPORIEVROSKTYFFOMIDLIGDLATSLFSANTSSSNIREINKH	500
	451	KELYLRSFFQETEVKDGKTYFKMHDL1HDLATSLFSANTSSSNIRBINKH	500
15	501	SYTHMMSIGFAEVVPFYTLPPLEKFISLRVLNLGDSTFNKLPSSIGDLVH	550
	501	SYTHMMSJGPAEVVFFYTLPPLEKFISLRVLNLGDSTFNKLPSSIGDLVH	550
	551	LRYLNLYGSGMRSLPROLCKLONLOTLDLOYCTKLCCLPKETSKLGSLRN	600
20	551	TEATUREAGEMEST REGITCRIVATED FÖLGER FEGSTERN	600
	601	LLIDGSQSLTCMPPRIGSLTCLRTLGQFVVGRKKGYQLGELGNLNLXGSX	650
25	103	LLLDGSQSLTCMPPRIGSLTCLKTLGQFVVGRKKGYQLGELGNLNLYGSI	650
23	651	KISHLERVENDEDAKEANLSAKONLESLSMSENNEGPRIYESEEVEVIJEA	700
	651	KISHLERVKNUMDAKEANLSAKONLHSLSMSWNNFGPHIYESEEVKVLEA	700
30	701	LEPHENLTSLKIYGFRGIBLPEWMNHSVLKNIVSILISNFRNCSCLPPFG	750
	701	LKPHSNLTSLKTYGFRCIHLPFNMNHSVLKNIVSILISNFRNCSCLPPFG	750
35	753	DIPCLESERLEMCSADVEYVEEVDIDVHSGFPTRIRFPSERKEDIWOFGS	800
	751	DLPCLESLEIAWGSADVEYVEEVDIDVHSGFPTRIRFPSLRKLDIWDFGS	800
	801	LKGLLKKEGEBOFPVLEEMI1HBCFFLTLSSNLRALFSLRICYNKVATSF	850
40	801	LKGLLKKEGEEOFPVLKEMIIHEOPFLYLSSNLRALTSLRICYNKVATSF	850
	851	PEEMFKNLANGKYLTISRCNWIKELPTSLASLNALKSLALESLP	894
45	851	PREMEKNIANIKYLTISRONNIKELPTSIASINAIKSIKIQICCALESIP	900
	895	EEGLESLSSLTELFVERCHMIKCLPEGLOHLTITSLKIRGCPOLIKRCE	944
	901	REGLEGLSSLIPELFVEHCRMLKCLPEGIQHLTTLTSLKIRGCPQL1KRCE	950
50	945	KGTGEDWHKTSHIPNVNIYI* 965	
	951	KG1GEDWHKISHTPNVN1YI* 971	

55 Example 6:

The following example shows a nucleic acid comparison between the gene 2 coding

regions from a disease resistant and disease susceptible variety. The top sequence is the gene 2 coding region from the resistant homolog. The bottom sequence is the gene 2 coding region

#### P03170US/WARF-0204

60439376.031003

from the susceptible 177013 homolog. Note that the susceptible homolog contains a C to G point mutation at position 1362 that creates a stop codon in second exon at Tyr454 (residue 454 of 970 total), creating a severely truncated protein, in addition to one mismatch (C to T) at codon 10 which doesn't change the amino acid and one sense mutation (T to C) at codon 22 which

5 alters valine to alanine.

		- 44 -	
	2295	GTFACTGAGCATFTCCATTCCAAAATATGGATTTGTGTCTCGGAAGATTT	2246
55	601	GTTACTGAGCATTTCCAAAATATGGATTTGTGTCTCGGAAGATTT	650
		GOCGATTAGGAAAAACGACTCTTGCCCAAATGCTCTTCAATGACCAGAGA	
50	551	GGGGATTAGGAAAAAGGACTCTTGCCCAAATGGTCTTCAATGACCAGAGA	600
		CARTGTTAGTGATGCCCARCACCTTTCAGTCCTCCCAATACTTGGTATGG	
		CARTCTTAGTGATGCCCAACACCTTTCAGTCCTCCCAATACTTGGTATGG	
45		GTTTATGGAAGAGACAAAGAGAAAGATCAGATAGTGAAAATCCTAATAAA	
	451	GTTTATGGAAGAGACAAAGAGAAGATGAGATAGTGAAAATCCTAATAAA	500
40	2495	AGAGACAAGCTGTTAGACGGGAAACAGGTTCTGTATTAACCGAACCGCAG	2446
		AGAGRCAAGCTGTTAGACGGGAAACACGTTCTGTATTAACCGAACCGCAG	
	2545	GGCAATTGCTGAGGAAAGAAATTTTCATTTGCACGAAAAAATTGTAG	2496
35	351	GGCAATTGCTGAGGAAAGAATTTTCATTTGCACGAAAAAATTGTAG	400
		TTCCCTCACAAGGTCGGGAAAAGGATGACCAAGTGATGAAAAAACTAAA	
30	303	TTCCCTCACAAGGTCGGGAAAAGGATGGACCAACTGATGAAAAAACTAAA	350
		CAAGAFFCTCCCAGTCTGAATATGGCCGTTATCATCCAAAGGTTATCCCT	
		CARGATTCTCCCAGTCTGAATATGGCCGTTATCATCCAAAGGTTATCCCT	
25		TOUTACATATGAAGTCGATGACATCTTGGATGACTATAAAACCAAGGCCA	
		TUCTACATATUAAGTCGATGACATCTTGGATGAATATAAAACCAAGGCCA	
20		THE HITTER STREET THE STREET TO THE STREET T	
		TTTCARGCATGTTTCTAGAATTCAAGCCGTGCTTGAAGATGCTCAGGAG AAGCAACTCAACAAGAGCTCTAGAAAATTGGTTGCAAAAACTCAATGC	
13		TTCAACCATCTTTCTACAATTCAAGCCGTCCTTGAAGATGCTCAGGAG !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!	
15		CAAAGGGAACTYGCATTGCTYTTCGCTTTTCAACATGAGTTCCAAAGGC	
		CAAAGGGAACTICTATTGCTTTTCGGTTTTCAAGATGAGTTCCAAAGGC	
10		ATGGCTGRAGCTTTCATTCAGTTCTGTTAGACAATCTCACTTCTTTCCT	
		ATGGCTGBAGCTTCATTCAACTTCTCCTAGACABTCTCACTTCTTTCCT	
	,	A DECOCRAÇÃO A COMPRIO A PRIOR A COMPONICIONA A DA A DA A DA CALA A DESCRIPTO DE PROPERTO	50

## P03170US/WARF-0204

# EGGLEG. GTEREFOR

	651	TOATGAGAAGAGGTTAATAAAGCCAATTGTAGAATCTATTGAAGGAAG	700
5	2245	TGATGAGAGAGGTTAATAAAGGCAATTGTAGAATCTATTGAAGGAAG	2196
	701	CACTACTTOGTGAGATGGACTTGGCTCCACTTCAAAAGAAGCTTCAGGAG	750
	2195	CACTACTTGGTGAGATGGACTTGGCTCCACTTCAAAAGAAGCTTCAGGAG	2146
10	751	TTGCTCAATGCAAAAAGATACTTGCTTGTCTTAGATGATCTTTGGAATGA	0.08
10	2145	TTCCTGAATGGAAAAGATACTTGCTTGTCTTAGATGATGTTTGGAATGA	2096
	801	AGATCAACAGAGTGGGCTAATTTAAGAGCAGTCTTGAAGTTTGGAGCAA	850
15	2095	ACATCABCAGBAGTGGGCTAATTTAAGAGCAGTCTTGBAGGTTCGAGCAA	2046
	851	GTGGTGCTTCTGTTCTAACCACTACTCGTCTTGAAAAGGTTGGATCAATT	900
20	2045	GTOGTGCTTCTGTTCTAACCACTACTCGTCTTGAAAAGGTTGGATCAATT	1996
	901	AYOGGABCATTGCAACCATATGAACTGTCAAACCTGTCTCAAGAAGATTG	950
	1995	ATGGGARCATTGCARCCATATGRACTGTCAAATCTGTCTCAAGAAGATTG	1946
25	951	TTGGTTCTTGTTCATCCAACGTGCATTTGGACACCAAGAAGAATAAATC	1000
	1945	TEGTTOTTETTCATGCAACGTGCATTTGGACACCAAGAAGAAATAAATC	1896
30	1001	CRANCTINGTGGCAATCGGAARGAGATTGTGAAAAAAGTGGTGGTGTG	1050
		CAAACCTTGTGGCAATCGGAAAGGAGATTGTGAAAAAAGTGGTGGTGTG	
		CCTCTAGCAGCGAAACTCTTGGAGGTATTTTGTGCTTCAAGAGAGAG	
35		CCTCTAGCAGCCAAAACTCTTGGAGGTATTTTGTCCTTCAAGAGAGAAGA	
		AAGAGCATEGGAACATETGAGAGACAGTCCGATTTGGAATTTGCCTCAAG	
40		AMGAGCATGGGAACATGTGAGAGACAGTCCGATTTGGAATTTGCCTCAAG	
		ATGAAAGTTCTATTCTGCCTGCCCTGAGGCTTAGTTACCATCAACTTCCA	
45		AYGAAGTTCTATTCTGCCTGCCCTGAGGCTTAGTTACCATCAACTTCCA	
43		CTTGATTFGAAACAATCCTTTGCGFATTGTGCGGTGTTCCCAAAGGATGC	
		CTTGATTTGAAACAATGCTTTGCGTATTGTGCGGTGTTCCCAAAGGATGC	
50		CARANTGANANAGABAGCTAATCTCTCTCTGGGTGGCGCATGGTTTC HILLI HILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIH	
		TTTTATCAAAAGGAAACATGGGCTACAGGATGTGGGCGATGAAGTATGG	
55		THITCHARGE AND A TRANSCORD TO THE CONTROL OF THE CO	
		AAGANTTATACTTGAGGTCTTTTTTCCAAGAGATTGAAGTTAAGATGG	
		AAAGAATTATAGTTGAGGTCTTTTTTCCAAGAGTTGAAGTTAAGATGG	
60		TARACTTATTTCARGATGCATGATCTCATCCATGATTTGGCAACATCTC	
		THE PROPERTY OF THE PROPERTY O	1430

- 45 -

P03170US	/WAI	RF-0204 69****S3	176	.Daloos
	1495	TAAAACTTATTTCAAGATGCATGATCTCATCCATGATTTGGCAACATCTC	1446	
5	1451	TGTTTTCAGCAAACACATCAAGCAGCAATATCCGTGAAATAAAT	1500	
	1445	TGTTTCAGCABACACATCAAGCAGCAATATCCGTGAAATAAATAAACAC	1396	
	1501	agttacacacatatgatgtccattggttecgccgaagtggtgtttttta	1550	
10	1395	AGTACAÇACATATGATGCCATTGCTTCCCCGAAGTGGTGTTTTTTA	1346	
	1551	CACTCTTCCCCCCTTGGAAAGTTTATCTCGTFAAGACTGCTTAATCTAG	1600	
	1345	CACTCTTCCCCCCTTGGAAAAGTTTATCTCGTTAAGAGTGCTTAATCTAG	1296	
15	1601	GTGATTCGACATTTAATAAGTTACCATCTTCCATTGGAGATCTAGTACAT	1.650	
	1295	GTGATTCGACATTTAATAAGTTACCATCTTCCATTGGAGATCTAGTACAT	1246	
20	1651	TRAGATACTTGRACCTGTATGGCAGTGGCATGCGTAGTCTTCCAARGCA	1700	
=-	1245	TTAGGATACTTOAACCTGTATGGCAGTGGCATGGGTAGTCTTGCAAAGCA	1196	
	1701	GTTATGCAAGCTTCABAATCTGCABACTCTTGATCTACAATATTGCACCA	1750	
25	1195	GTTATGCAAGCTTCAAAATCTGCAAACTCTTGATCTACAATATTGCACCA	1146	
	1751	AGCTTTGTTGTTGCCAAAGGAACAAGTAAACTTGGTAGTCTCCGAAAT	1800	
30	1145	AGCITTGITGITGCCAAAGAAACAAGTAAACTTGGTAGTCTCCGAAAT	1096	
	1801	CTTTTACTIGATGCTAGCCAGTCATTGACTTGTATGCCACCAAGGATAGG	1850	
		CTITTACTTGATGGTAGCCAGTCATTGACTTGTATGCCACCAAGGATAGG		
35	1851	AT'ATTGACATGCCTTARGACTCTAGGTCAATTTGTTGGTAGGAAG	1900	
		ATCATTGACATGCCTTAAGACTCTAGGTCAATTTGTTCTTGGAAGGAA		
40		AGGTTATCAACTTGGTGAACTAGGAAACCTARATCTCTRTGGCTCAATT		
		ARGITTATCHACTTGGTGRACTRGGARACCTRATCTCTATGGCTCAATT		
		AAAATCTCGCATCTTGAGRGAGTGAAGAATGATGTGGACGCAAAAGAAGC		
45		AAAATCTCGCATCTTGAGAGGGTGAAGKATGNTAAGGACGCAAAAGAAGC		
		CARTTERTCTGCAAAAGGAATCTGCATTCTTTAAGCATGAGTTGGAWA		
50		CAATTENUTGCAAAAGGGRATCTGCATTCTTTAAGCRTGAGTTGGRATR		
		ACTTTGGACCACATATATATGAATCAGAGGAGTTAAAGTCCTTGAAGCC		
55		ACTITIGGACCACATATATATGAATCAGAAGAAGTTAAAGTGCTTGAAGCC CTCAAACCACACTCCAATCTGACTTCTFTAAAAATCTATGGCTTCAGAGG		
		1		
60		CTCAARCCACRCTCCAATCTGECTTCTTTAAAAATCTATGGCTTCAGEGG AATCCATCTCCCAGEGTGGATGAATCACTCAGTATGAAAAATATTGTCT		
		HILLIELLE HILLIE		
	••	TOTAL	0110	

- 46 -

#### P03170US/WARF-0204

# 50439376.011003

		CTATTCTAATTAGCAACTTCAGAAACTGCTCATGCTTACCACCCTTTGGT	
5		GATCTGCCTTGTCTAGAAAGTCTAGAGTTACACTGGGGGTCTGCGGATGT	
	645	GATCTGCCTTCTTGGAAAGTCTAGACTTACACTGGGGGTCTGCGGATGT	596
10		GGACTATOTIGARGAGTIGATATTGATOTCATTCTGGATTCCCCACAA	
		GGAGTATGTTGAAGAAGTGGATATTGATGTTCATTCTGGATTCCCCACAA	
15		GAATAGGTTTCCATCCTTGAGGAAACTTGATATATGGGACTTTGGTAGT 	
	2401	CTSABAGGATTGCTGABABAGGABGGABGAGGCBATTCCCTGTGCTTGA	2450
20	495	CTCAAAGCATTGCTGAAAAAGGAAGGAAGAGCAATTCCCTGTGCTTGA	446
20	2451	AGRICATION CANTER CONTROL OF THE CONT	2500
	445	AGAGATGATAATTCACGAGTGCCCTTTCTGACCCTTTCTCTAATCTA	396
25	2501	GSGCTCTTACTTCCCTCAGAATTTGCTATAATAAAGTAGCTACTTCATTC	2550
	395	GGGCTCTTACTTCCCTCAGAATTTGCTATAATAAAGTAGCTACTTCATTC	346
30	2551	CCAGAAGAGÁTGTTCAAAAACCTTGCAAATCTCAAATACTTGACAATCTC	2600
	345	CCAGRAGAGATGTCARANACCTTGCARATCTCARATACTTGACAATCTC	296
35		TCCGTGCANTAATCTCAAAGAGCTGCCTACCAGCTTGGCTAGCTGGATG	
		CTTTGANAGTCTAANAATTCAATTGTGTTGGGCACTAGAGAGTCTCCCT	
	245	CTTTGAAAAGTCTAGCACTAGAGAGTCTCCCT	214
40	2701	GAGGAAGGCTGGAAGGTTATCTTCACTCACAGAGTTATTTGTTGAACA	2750
	213	GAGGAAGGCTGGAAGGTTATCTTCACCTCACAGAGTTATTTGTTGAACA	164
45	2751	CTGTABCATGCTABAATGTTTACCAGAGGGATTGCAGCACCTAACAACCC	2800
	163	CTGTAACATGCTGAAATGTTTACCAGAGGGATTGCAGCACCTAACAACCC	114
50	2801	TCACAAGTTTAAAAATTCGGGGATGTCCACAACTGATCAAGCGGTGTGAG	2850
	113	TCACAAGTTTAAAAATTCGGGGATGTCCACAACTGATCAAGCGGTGTGAG	64
55	2851	AAGGGAATAGGAGAAGACTGGCACAAAATTCTCACATTCCTAATGTGAA	2900
		AAGGGAATAGGAGAGACTGCCACAAAATTTCTCACATTCCTAATCTGA	14
	2901	TATATATATTAA 2913	
60	1.3	TATATATATTAA 1	

- 47 -